```
                          20                              40
CTT TCT ATT TGG TTA ACC ATG GCT CAT AAC TTT CGT CAT CCT TTC TTC
Leu Ser Ile Trp Leu Thr Met Ala His Asn Phe Arg His Pro Phe Phe>

                60                              80
CTT TTC CAA CTT TTA CTC ATT ACT GTC TCA CTA ATG ATC GGT AGC CAC
Leu Phe Gln Leu Leu Leu Ile Thr Val Ser Leu Met Ile Gly Ser His>

  100                           120                           140
    *
ACC GTC TCG TCA GCG GCT CGA CAT TTA TTC CAC ACA CAA ACA ACC TCA
Thr Val Ser Ser Ala Ala Arg His Leu Phe His Thr Gln Thr Thr Ser>

                    160                             180
TCA GAG CTG CCA CAA TTG GCT TCA AAA TAC GAA AAG CAC GAA GAG TCT
Ser Glu Leu Pro Gln Leu Ala Ser Lys Tyr Glu Lys His Glu Glu Ser>

        200                             220                             240
          *
GAA TAC AAA CAG CCA AAA TAT CAT GAA GAG TAC CCA AAA CAT GAG AAG
Glu Tyr Lys Gln Pro Lys Tyr His Glu Glu Tyr Pro Lys His Glu Lys>

                          260                             280
CCT GAA ATG TAC AAG GAG GAA AAA CAA AAA CCC TGC AAA CAT CAT GAA
Pro Glu Met Tyr Lys Glu Glu Lys Gln Lys Pro Cys Lys His His Glu>

              300                             320
                *
GAG TAC CAC GAG TCA CGC GAA TCG AAG GAG CAC GAA GAG TAC GAT AAA
Glu Tyr His Glu Ser Arg Glu Ser Lys Glu His Glu Glu Tyr Asp Lys>

  340                           360                           380
GAA AAA CCC GAT TTC CCC AAA TGG GAA AAG CCT AAA GAG CAC GAG AAA
Glu Lys Pro Asp Phe Pro Lys Trp Glu Lys Pro Lys Glu His Glu Lys>

                    400                             420
```

FIGURE 1A

26027 6604860

```
                          *
CAC GAA GTC GAA TAT CCG AAA ATA CCC GAG TAC AAG GAC AAA CAA GAT
His Glu Val Glu Tyr Pro Lys Ile Pro Glu Tyr Lys Asp Lys Gln Asp>

      440                         460                         480
GAG AAT AAG AAA CAT AAA GAT GAA GAG TGC CAG GAG TCA CAC GAA TCG
Glu Asn Lys Lys His Lys Asp Glu Glu Cys Gln Glu Ser His Glu Ser>

                        500                         520
                          *
AAA GAG CAC GAA GAG TAC GAG AAA GAA AAA CCC GAT TTC CCC AAA TGG
Lys Glu His Glu Glu Tyr Glu Lys Glu Lys Pro Asp Phe Pro Lys Trp>

            540                         560
GAA AAG CCT AAA GGG CAC GAG AAA CAT AAA GCC GAA TAT CCG AAA ATA
Glu Lys Pro Lys Gly His Glu Lys His Lys Ala Glu Tyr Pro Lys Ile>

  580                         600                         620
                            *
CCT GAG TGC AAG GAA AAA CTA GAT GAG GAT AAG GAA CAT AAA CAT GAG
Pro Glu Cys Lys Glu Lys Leu Asp Glu Asp Lys Glu His Lys His Glu>

                  640                         660
TTC CCA AAG CAT GAA AAA GAA GAG GAG AAG AAA CCT GAG AAA GGC ATA
Phe Pro Lys His Glu Lys Glu Glu Glu Lys Lys Pro Glu Lys Gly Ile>

       680                         700                         720
                                    *
GTA CCC TGA GTG GGT TAA AAT GCC TGA ATG GCC GAA GTC CAT GTT TAC
Val Pro *** Val Gly *** Asn Ala *** Met Ala Glu Val His Val Tyr>

                        740                         760
TCA GTC TGG CTC GAG CAC TAA GCC TTA AGC CAT ATG ACA CTG GTG CAT
Ser Val Trp Leu Glu His *** Ala Leu Ser His Met Thr Leu Val His>

            780                         800
                                          *
```

FIGURE 1B

Z6E02T' 60h8680

```
GTG CCA TCA TCA TGC AGT AAT TTC ATG GGA TAT TGT AAT TAT ATT GTT
Val Pro Ser Ser Cys Ser Asn Phe Met Gly Tyr Cys Asn Tyr Ile Val>

  820                         840                         860
AAT AAA AAA GAT GGT GAG TGG GAA ATG TGT GTG TGC ATT CAT CCA TGA
Asn Lys Lys Asp Gly Glu Trp Glu Met Cys Val Cys Ile His Pro ***>

                    880                         900
                                                 *
GCA ATG CTG AAT CTC TTT GCA TGC ATA GAG ATT CTG AAT GGT TAT AGT
Ala Met Leu Asn Leu Phe Ala Cys Ile Glu Ile Leu Asn Gly Tyr Ser>

       920                         940                         960
TTA TGT TAT ATC GTT TGT TCT AGT GAA ATT AAT TTT GAA TGT TGT ATG
Leu Cys Tyr Ile Val Cys Ser Ser Glu Ile Asn Phe Glu Cys Cys Met>

TAA TGT T
*** Cys Xxx>
```

FIGURE 1C

```
                    20                  40                  60
ACTAAAGGGA ACAAAAGCTG GAGCTCCACC GCGGTGGCGG CCGCTCTAGA ACTAGTGGAT

                    80                 100                 120
                                        *
CCCCCGTGGA CTAAACAAAA CATGGGAAGA TTTGCTGTAA AAAAATAAAA GAAGCTTACT

                   140                 160                 180
CAATAACACT TTGTGAATTG TATACAAAAG ACTCAATGAA AAACAATAAC TCAATACACT

                   200                 220                 240
                    *
TTTTTTCACT GATTTACATC CTTTATATAG GCTGAAACTA CAACAACTTT AGCTAAAAAA

                   260                 280                 300
                                                            *
ATAGGATAAC CTAATAGCAA AATCACAATC AGATATTAAA CCATGATTTT AGCTAACCAT

                   320                 340                 360
TTAACAACTT TATTGAAACT AATTTGAATA TTTCATCTGC TGATATGCCC AAGATTTTAG

                   380                 400                 420
                                        *
GCCACTAACC GATTTGGTGG TGAACTTTAA CATGTCATGC ATTTGTAACT GTTTGAAACA

                   440                 460                 480
AGTTTTTTGC ATTATTTTAC TATATGAACT GTTTGATTAG GTTGAGTTAC ACACTGAGCT

                   500                 520                 540
                    *
TGTAAGCTCA CTCAAATTTT TCTAATTTCT AAGGTGATCA GCAAACTTAG GACCGGGCGG

                   560                 580                 600
                                                            *
CGTACGAGAG CTCGGATTGA TTTTCTAGTT AATAAATAAG ACGATTTATG TTTTTAAACT
```

Figure 2A

26E02F"660h8680

```
                    620                 640                 660
ATTATGGACT TTTTGGACTA TGTAACTGTT TGGGACTTTA TTTTTGTTTT TTATTTGCTT

                    680                 700                 720
                                         *
TTTTTGGATT TAGTAATTAT TATTTTTAAA CTGCAAAATT ATATGTTTTT ACAAACTAAG

                    740                 760                 780
TCACAGTTTT CAAAATTCCA TAACTTAGAA TTTTTCGCTG CAAAATAAAG TAATCATTTA

                    800                 820                 840
                     *
AGTGTTTTTT CTGTAATAAA ATAAATAAAT AATTTTAACG AGTATTTTCC TAAAAATTGG

                    860                 880                 900
                                                             *
AAATTGATTT ACCAAAATTA GTATGTCAAA ACACATGTTT ATATGTTACA GGGCGATATC

                    920                 940                 960
GTCTAGGCAA ATAACATCTA GGCGGGGTTT GGAGTGTTAC AGGGCGAGTG GGCTCATTTT

                    980                1000                1020
                                        *
GAGTAAGTAT AGTTAGGGCC GAGTTTTAGA TTGCATATTC AAGGTCAAAG ATTTTGTAAA

                   1040                1060                1080
CTTCGATGAA TGATATGTAT GATTGTCCGA TTAACGAAAT ATGTTTTTTT CTTTTGTGTG

                   1100                1120                1140
                     *
TGTTTTATCT CGTGTGATAA GTATATAGTA TGTTTTATTC CAATTCTTAT GGCATGTGAC

                   1160                1180                1200
                                                            *
ATTGTGGCTA TTCTAATTAA ATTGATTTGT TATTATTGAA ATCTGATGCA TCTGTTCTAC

                   1220                1240                1260
```

Figure 2B

```
AAAGCATGGA ATCTCATGCC TACTGCTTTC TGTTAAAGAT ACGATTGCAA GTTTAACATG

                  1280                  1300                  1320
                                         *
CTTACTATTT TGATTTTGTC CTTGCATGCT ATGTCACATT ACATGGGGTT GGGATGATAT

                  1340                  1360                  1380
GGTAAGGAGG AAGTTTTGAC AGTTTAATGA TTTGCACTAT CTGGTGGTTT AACCACATAT

                  1400                  1420                  1440
                   *
TTGTTATGGC ATCTTGACTG CGGTTATGGT GGCTCGACCG CCCATATCTG TTCTGGAAAT

                  1460                  1480                  1500
                                                               *
TTATCTGTGA CTCTGGTGGC ATTGTCTACA ATTATTTGTT GGTGTGTTTT GGATGGACGA

                  1520                  1540                  1560
GTCGTGGGGA ACTCTATTTG GTGTGTTGCG GAGTTGGGTA GGAAATTTTC GAAAAAAATT

                  1580                  1600                  1620
                                         *
TGCATTGTGT TTTTCTGAAA AATATTGCAT TAACATAATC ATGCATTCTC AATTTTGGTC

                  1640                  1660                  1680
AATTGAACGT TATAAAATTC TCTATGATAT CCTGATCTGT TTATTACATT ATATGTGTTT

                  1700                  1720                  1740
                   *
ATGCTTGAGT TAAGTCAAAC ATTGAGATTC ATAGCTCACC CAATTATTTA ATCATTTCAG

                  1760                  1780                  1800
                                                               *
GCAATCTGCA GACTTAGGAT TGGATGGCGT TCAGGAGCTT GGATTGGTTT TCTCACATCA

                  1820                  1840                  1860
TATTTTATTA AATAATTATT AATTAAAATT TATGGACTTT TGGACTGTCT GACTAATTTT
```

Figure 2C

```
                1880                1900                1920
                                     *
CAGAATTTTA TTTTGGTTTT GGGTTTTGTT GAATTTTTTA GATAATTATT TTAAATATTC

                1940                1960                1980
TGCATAATTT TTCTGTTATT TGAAAAGGAT GTTCGAATTT TTTTTCAAAA TTGAAACGTT

                2000                2020                2040
                 *
TAAGAATTTT TACTACTGCA AATTCAGAAT AAGTGAATTT GTTTTTTAGA AAGATTAAAT

                2060                2080                2100
                                                         *
AAGTTAGTAT TACGATTTTT AGTTTGATTT GGTGGAAAGT AATGTATGTT TTTGAACATA

                2120                2140                2160
ATTATTTGAC AATAATTAAG TTTTCTAGGG AATAAACGGA AATATCTTCT TCTTTTTTGT

                2180                2200                2220
                                     *
AAAATTACTA ATGCAAGAAC AAACAACGTT TTGGGGAGCA AATAATCTAG CTTTAAGTAG

                2240                2260                2280
TCAGTGTAAC TCTCAAAATC TGGTCATAAC TTCTAGGCTG AGTTTGCTGT GCTACAGTAG

                2300                2320                2340
                 *
TAAGTCTATA GAAACTTACC TGACAAAACG ACATGACGTC AGGGTCGAAT CTACAACTTT

                2360                2380                2400
                                                         *
TCCTTTTTCT TCAATTAACA TATGGTTGAT TCAAGTTCCG ATCTATAATA ATTTATTACG

                2420                2440                2460
ATTTATCAAT TTCAATTACC TTATATCATC CTATTATAAA TATAAGTCAG TTCAATTCAG
```

Figure 2D

26027 6604680

```
                2480                2500                2520
                                     *
TTTTCGAAAG TTCCCAAAAA TTTTGAATTT TATTAAATTT ATTCCCTAAA ACCGAAATAG

                2540                2560                2580
TTATATCTTT CAAATTTAAG TTTCATTTTT CAATCCGATT TCAATTTCAT CCTTTTATAA

                2600                2620                2640
                 *
CTCTCTATTA TCTATAATTA CATAAATTTC AAATTAATTT TGAAATATTT ACACTTTAGT

                2660                2680                2700
                                                         *
CCCTAAGTTC AAAACTATAA ATTTTCACTT TAGAAATTAA TCATTTTTCA CATCTAAGCA

                2720                2740                2760
TCAAATTTAA CCAAATGACA CAAATTTCAT GATTAGTTAG ATCAAGCTTT TGAGTCTTCA

                2780                2800                2820
                                     *
AAACATAAAA ATTACAAAAA AAAAACAAAC TTAAAATCAT TTATCAATTT GAACAACAAA

                2840                2860                2880
GCTTGGCCGA ATGCTAAGAG CTTAAAAATG GCTTCTTTTG TTTCTTTTTG TTGCAAACGG

                2900                2920                2940
                 *
TGGAGAGAAG AGGGAAATGA AGATTGACCA TATTTTTTTA TTATGTTTTA ACATATAATA

                2960                2980                3000
                                                         *
TTAATAATTT AATCATAATT ATACTTTGGT GAATGTGACA GTGGGGAGAT ACGTAAAGTA

                3020                3040                3060
TTTTAACATT ATACTTTTTG CAAGCAGTTG GCTGGTCTAC CCAAGAGTGA TCAAAGTTTG

                3080                3100                3120
```

Figure 2E

```
                                                  *
AGCTGCCTTC AATGAGCCAA TTTTTGCCCA TAATGGATAA AGGCAATTTG TTTAGTTCAA

                3140                3160                3180
CTGCTCACAG AATAATGTTA AAATGAAATT AAAATAAGGT GGCCTGGTCA CACACACAAA

                3200                3220                3240
                 *
AAAAAACTAA TGTTGGTTGG TTGAATTTTA TATTACGGAA TGTAATATTA TATTTTAAAA

                3260                3280                3300
                                                             *
TAAAATTATG TTATTTAGAT TCTTAATATT TTGGAGCATT CCATACTATA ATTTCGTAAC

                3320                3340                3360
ATAATATTAA AATATAGTAA TATAAAGTGT AATTAACTTT AAATTACAAG CATAATATTA

                3380                3400                3420
                                     *
AATTTTGAAT CAATTAATTT TTATTTCTAT TATTTTAATT AATTTAGTCT ATTTTTTCAA

                3440                3460                3480
AATAAAATTT AAATCTAAAT AAAAATAATT TTTCCTTAAT GTTGAAACAA CTCATGTTAT

                3500                3520                3540
                 *
ACTTCAAAAT TATAAGTATT ATATTTACCT TGATGATTTA TTTATTAGTA TATTAATTCT

                3560                3580                3600
                                                             *
GATTATAATT ATGGTGGGAT ACAATCGCTT TCCACTAAAT ATTTTAACTA TGATTTATAA

                3620                3640                3660
ATTTATTTCA ACATCGTATA TTTACTTATT AATACATAAT TTATCATAAT TTTATGGAAA

                3680                3700                3720
                                     *
```

Figure 2F

26027 6604680

```
TTGAGACCAA GAAACATTAA GAGAACAAAT TCTATAACAA AGACAATTTA GAAAAAAATG

                  3740                  3760                  3780
TACTTTTAGG TAATTTTAAG TACTCTTAAC CAAACACAAA AATTCAAATC AAATGAACTA

                  3800                  3820                  3840
                    *
AATAAGATAA TATAACATAC GGAACATCTT ACTTGTAATC TTACATTCCC ATAATTTTAT

                  3860                  3880                  3900
                                                                *
TATGAAAAAT AATCTTATAT TACTCGAACT AAATGTTGTC ACAAATTATT ATCTAAATAA

                  3920                  3940                  3960
AGAAAAACAC TTAATTTTTA TAACATTTTT TCATATATTT GAAAGATTAT ATTTTGTATA

                  3980                  4000                  4020
                                          *
TTTACGTAAA AATATTTGAC ATAGATTGAG CACCTTCTTA ACATAATCCC ACCATAAGTC

                  4040                  4060                  4080
AAGTATGTAG ATGAGAAATT GGTACAAACA ACGTGGGGCC AAATCCCACC AAACCATCTC

                  4100                  4120
                    *
TCATTCTCTC CTATAAAAGG CTTGCTACAC ATAGACAACA ATCCACACA C AAA TAC
                                                        <Phe Val

  4140                  4160                  4180
 ACG TTC TTT TCT TTC TAT TTG ATT AAC CAT GGC TCA TAG CAT TCG TCA
<Arg Glu Lys Arg Glu Ile Gln Asn Val Met Ala *** Leu Met Arg ***

                  4200                  4220
                    *
 CCC TTT CTT CCT TTT CCA ACT TTT ACT CAT AAG TGT CTC ACT AGT GAC
<Gly Lys Lys Arg Lys Trp Ser Lys Ser Met Leu Thr Glu Ser Thr Val
```

Figure 2G

```
      4240                          4260                          4280
 CGG TAG CCA CAC TGT TTC GGC AGC GGC TCG ACG TTT ATT CGA GAC ACA
<Pro Leu Trp Val Thr Glu Ala Ala Ala Arg Arg Lys Asn Ser Val Cys

                        4300                          4320
                          *
 AGC AAC CTC ATC AGA GCT CCC ACA ATT GGC TTC AAA ATA CGA AAG CAC
<Ala Val Glu Asp Ser Ser Gly Cys Asn Ala Glu Phe Tyr Ser Leu Val

            4340                          4360
 GAG AGT CTG AAT ACG AAA AGC CAG AAT ACA AAC AGC CAA AGT ATC ACG
<Leu Thr Gln Ile Arg Phe Ala Leu Ile Cys Val Ala Leu Thr Asp Arg

  4380                          4400                          4420
                                  *
 AAG AGT ACT CAA AAC TTG AGA AGC CTG AAA TGC AAA AGG AGG AAA AAC
<Leu Thr Ser Leu Val Gln Ser Ala Gln Phe Ala Phe Pro Pro Phe Val

                    4440                          4460
 AAA AAC CCT GCA AAC AGC ATG AAG AGT ACC ACG AGT CAC ACG AAT CAA
<Phe Val Arg Cys Val Ala His Leu Thr Gly Arg Thr Val Arg Ile Leu

      4480                          4500                    4520
                                      *
 AGG AGC AAA AAG AGT ACG AGA AAG AAA ATC TCGACGAA TTCCCCCGGG
<Pro Ala Phe Leu Thr Arg Ser Leu Phe Asp

                    4540                    4560                    4580
CGTCGACGGC TAGCGAAGAT CTTCGGGCCC GTCGAGCCTT GAATCATATG ACACTGGTGC

                    4600                    4620                    4640
                      *
ATGTGCCATC ATCATGCAGT AATTTCATGG TATATCGTAA TATATAGTTA ATAAAAAAGA

                    4660                    4680                    4700
                                                                      *
TGGTGATTGG GAAATGTGTG TGTGCATTCC TCCATGCACT AATGGTGAAT CTCTTTGCAT
```

Figure 2H

```
                    4720                    4740                    4760
ACATAGAAAT TCTAAATGGT TATAGTTTAT GTTATAGTGT ATGTTGTAGT GAAATTAATT

                    4780                    4800                    4820
                                             *
TTAAATGTTG TATCTAATGT TAACATCACT TGGCTTGATT TATGTTATGT TATGTATTTT

                    4840                    4860                    4880
ACTTTAATGA TATTGCATGT ATTGTTAATT TAACATTGCT TGATCATTAT ACTCTTCTAC

                    4900                    4920                    4940
                     *
TATTAATTAT AAATGGCACT GTTTTGTTTA AACTTTTTAC AAGTTAAGAC ATGTATAAAT

                    4960                    4980                    5000
                                                                     *
ATATGACAAT ATAATTACAG GTTTTAGTTC AATGTTAGCT ATCTTAGTAT GTTATTGATG

                    5020                    5040                    5060
ATCTTAATTA CATTTAAACA AATTCCACTT AAAATTTTAA TAAATAATAA CAAATAATTA

                    5080                    5100                    5120
                                             *
TTGTAATATA ATACATTAAA TGCAACAAAA AATGAAATAA ATAAAATAAA ATAGCAAATA

                    5140                    5160                    5180
ATTGTTATAA TATTGTAATA TAATATGTAC CATATTCTTA ACTGAAATAG GGTCTAACCT

                    5200                    5220                    5240
                     *
ATAATCCCTA AAATTTCAGT TTAAATATTT TTATACCTAC CATATTATTA GAACTCTTTT

                    5260                    5280                    5300
                                                                     *
TAAATATATT AAAATTTTAA TTATACCAAT TTAATTAAAC TATTAATTAT CTTAACTAAA
```

Figure 2I

26027 6604680

```
                    5320                5340                5360
ATCTAAAATT TTATTTAACC TATTAATAAA TTCCTAATTA TCTTATCTAA TTTAAAACTC

                    5380                5400                5420
                                        *
TAATTATCCT AATTTAATTT AAATTCTTAA TTATCTTAAT TTGTAACCTC CTCCACCCAG

                    5440                5460                5480
CTAGATGCTG GACCCGAATC CGGGAGATTA CATCGGCCAT TGAGATGGCG TGATCAGGGT

                    5500                5520                5540
                     *
TTGGCGCGCC GGTACCCAAT TCGCCCTATA GTGAGTTCGT ATTACGCGCG CTCACTGCGT

CCGGTTT
```

Figure 2J

26202T "60h8680

```
                    20                  40                  60
ACTAAAGGGA ACAAAAGCTG GAGCTCCACC GCGGTGGCGG CCGCTCTAGG ATCCCCCGTG

                    80                 100                 120
                                        *
GACTAAACAA AACATGGGAA GATTTGCTGT AAAAAAATAA AAGAAGCTTA CTCAATAACA

                   140                 160                 180
CTTTGTGAAT TGTATACAAA AGACTCAATG AAAAACAATA ACTCAATACA CTTTTTTTCA

                   200                 220                 240
                    *
CTGATTTACA TCCTTTATAT AGGCTGAAAC TACAACAACT TTAGCTAAAA AAATAGGATA

                   260                 280                 300
                                                            *
ACCTAATAGC AAAATCACAA TCAGATATTA AACCATGATT TTAGCTAACC ATTTAACAAC

                   320                 340                 360
TTTATTGAAA CTAATTTGAA TATTTCATCT GCTGATATGC CCAAGATTTT AGGCCACTAA

                   380                 400                 420
                                        *
CCGATTTGGT GGTGAACTTT AACATGTCAT GCATTTGTAA CTGTTTGAAA CAAGTTTTTT

                   440                 460                 480
GCATTATTTT ACTATATGAA CTGTTTGATT AGGTTGAGTT ACACACTGAG CTTGTAAGCT

                   500                 520                 540
                    *
CACTCAAATT TTTCTAATTT CTAAGGTGAT CAGCAAACTT AGGACCGGGC GGCGTACGAG

                   560                 580                 600
                                                            *
AGCTCGGATT GATTTTCTAG TTAATAAATA AGACGATTTA TGTTTTTAAA CTATTATGGA
```

Figure 3A

```
                    620                 640                 660
CTTTTTGGAC TATGTAACTG TTTGGGACTT TATTTTTGTT TTTTATTTGC TTTTTTTGGA

                    680                 700                 720
                                         *
TTTAGTAATT ATTATTTTTA AACTGCAAAA TTATATGTTT TTACAAACTA AGTCACAGTT

                    740                 760                 780
TTCAAAATTC CATAACTTAG AATTTTTCGC TGCAAAATAA AGTAATCATT TAAGTGTTTT

                    800                 820                 840
                     *
TTCTGTAATA AAATAAATAA ATAATTTTAA CGAGTATTTT CCTAAAAATT GGAAATTGAT

                    860                 880                 900
                                                             *
TTACCAAAAT TAGTATGTCA AAACACATGT TTATATGTTA CAGGGCGATA TCGTCTAGGC

                    920                 940                 960
AAATAACATC TAGGCGGGGT TTGGAGTGTT ACAGGGCGAG TGGGCTCATT TTGAGTAAGT

                    980                1000                1020
                                         *
ATAGTTAGGG CCGAGTTTTA GATTGCATAT TCAAGGTCAA AGATTTTGTA AACTTCGATG

                   1040                1060                1080
AATGATATGT ATGATTGTCC GATTAACGAA ATATGTTTTT TTCTTTTGTG TGTGTTTTAT

                   1100                1120                1140
                     *
CTCGTGTGAT AAGTATATAG TATGTTTTAT TCCAATTCTT ATGGCATGTG ACATTGTGGC

                   1160                1180                1200
                                                             *
TATTCTAATT AAATTGATTT GTTATTATTG AAATCTGATG CATCTGTTCT ACAAAGCATG

                   1220                1240                1260
```

Figure 3B

```
GAATCTCATG CCTACTGCTT TCTGTTAAAG ATACGATTGC AAGTTTAACA TGCTTACTAT

                  1280                  1300                  1320
                                         *
TTTGATTTTG TCCTTGCATG CTATGTCACA TTACATGGGG TTGGGATGAT ATGGTAAGGA

                  1340                  1360                  1380
GGAAGTTTTG ACAGTTTAAT GATTTGCACT ATCTGGTGGT TTAACCACAT ATTTGTTATG

                  1400                  1420                  1440
                   *
GCATCTTGAC TGCGGTTATG GTGGCTCGAC CGCCCATATC TGTTCTGGAA ATTTATCTGT

                  1460                  1480                  1500
                                                               *
GACTCTGGTG GCATTGTCTA CAATTATTTG TTGGTGTGTT TTGGATGGAC GAGTCGTGGG

                  1520                  1540                  1560
GAACTCTATT TGGTGTGTTG CGGAGTTGGG TAGGAAATTT TCGAAAAAAA TTTGCATTGT

                  1580                  1600                  1620
                                         *
GTTTTTCTGA AAAATATTGC ATTAACATAA TCATGCATTC TCAATTTTGG TCAATTGAAC

                  1640                  1660                  1680
GTTATAAAAT TCTCTATGAT ATCCTGATCT GTTTATTACA TTATATGTGT TTATGCTTGA

                  1700                  1720                  1740
                   *
GTTAAGTCAA ACATTGAGAT TCATAGCTCA CCCAATTATT TAATCATTTC AGGCAATCTG

                  1760                  1780                  1800
                                                               *
CAGACTTAGG ATTGGATGGC GTTCAGGAGC TTGGATTGGT TTTCTCACAT CATATTTTAT

                  1820                  1840                  1860
TAAATAATTA TTAATTAAAA TTTATGGACT TTTGGACTGT CTGACTAATT TTCAGAATTT
```

Figure 3C

```
                1880                1900                1920
                                     *
TATTTTGGTT TTGGGTTTTG TTGAATTTTT TAGATAATTA TTTTAAATAT TCTGCATAAT

                1940                1960                1980
TTTTCTGTTA TTTGAAAAGG ATGTTCGAAT TTTTTTTCAA AATTGAAACG TTTAAGAATT

                2000                2020                2040
                 *
TTTACTACTG CAAATTCAGA ATAAGTGAAT TTGTTTTTTA GAAAGATTAA ATAAGTTAGT

                2060                2080                2100
                                                         *
ATTACGATTT TTAGTTTGAT TTGGTGGAAA GTAATGTATG TTTTTGAACA TAATTATTTG

                2120                2140                2160
ACAATAATTA AGTTTTCTAG GGAATAAACG GAAATATCTT CTTCTTTTTT GTAAAATTAC

                2180                2200                2220
                                     *
TAATGCAAGA ACAAACAACG TTTTGGGGAG CAAATAATCT AGCTTTAAGT AGTCAGTGTA

                2240                2260                2280
ACTCTCAAAA TCTGGTCATA ACTTCTAGGC TGAGTTTGCT GTGCTACAGT AGTAAGTCTA

                2300                2320                2340
                 *
TAGAAACTTA CCTGACAAAA CGACATGACG TCAGGGTCGA ATCTACAACT TTTCCTTTTT

                2360                2380                2400
                                                         *
CTTCAATTAA CATATGGTTG ATTCAAGTTC CGATCTATAA TAATTTATTA CGATTTATCA

                2420                2440                2460
ATTTCAATTA CCTTATATCA TCCTATTATA AATATAAGTC AGTTCAATTC AGTTTTCGAA
```

Figure 3D

```
                2480                2500                2520
                                     *
AGTTCCCAAA AATTTTGAAT TTTATTAAAT TTATTCCCTA AAACCGAAAT AGTTATATCT

                2540                2560                2580
TTCAAATTTA AGTTTCATTT TTCAATCCGA TTTCAATTTC ATCCTTTTAT AACTCTCTAT

                2600                2620                2640
                     *
TATCTATAAT TACATAAATT TCAAATTAAT TTTGAAATAT TTACACTTTA GTCCCTAAGT

                2660                2680                2700
                                                         *
TCAAAACTAT AAATTTTCAC TTTAGAAATT AATCATTTTT CACATCTAAG CATCAAATTT

                2720                2740                2760
AACCAAATGA CACAAATTTC ATGATTAGTT AGATCAAGCT TTTGAGTCTT CAAAACATAA

                2780                2800                2820
                                     *
AAATTACAAA AAAAAAACAA ACTTAAAATC ATTTATCAAT TTGAACAACA AAGCTTGGCC

                2840                2860                2880
GAATGCTAAG AGCTTAAAAA TGGCTTCTTT TGTTTCTTTT TGTTGCAAAC GGTGGAGAGA

                2900                2920                2940
                     *
AGAGGGAAAT GAAGATTGAC CATATTTTTT TATTATGTTT TAACATATAA TATTAATAAT

                2960                2980                3000
                                                         *
TTAATCATAA TTATACTTTG GTGAATGTGA CAGTGGGGAG ATACGTAAAG TATTTTAACA

                3020                3040                3060
TTATACTTTT TGCAAGCAGT TGGCTGGTCT ACCCAAGAGT GATCAAAGTT TGAGCTGCCT

                3080                3100                3120
```

Figure 3E

```
                                                    *
TCAATGAGCC AATTTTTGCC CATAATGGAT AAAGGCAATT TGTTTAGTTC AACTGCTCAC

                3140                3160                3180
AGAATAATGT TAAAATGAAA TTAAAATAAG GTGGCCTGGT CACACACACA AAAAAAAACT

                3200                3220                3240
                  *
AATGTTGGTT GGTTGAATTT TATATTACGG AATGTAATAT TATATTTTAA AATAAAATTA

                3260                3280                3300
                                                          *
TGTTATTTAG ATTCTTAATA TTTTGGAGCA TTCCATACTA TAATTTCGTA ACATAATATT

                3320                3340                3360
AAAATATAGT AATATAAAGT GTAATTAACT TTAAATTACA AGCATAATAT TAAATTTTGA

                3380                3400                3420
                                      *
ATCAATTAAT TTTTATTTCT ATTATTTTAA TTAATTTAGT CTATTTTTTC AAAATAAAAT

                3440                3460                3480
TTAAATCTAA ATAAAAATAA TTTTTTCCTTA ATGTTGAAAC AACTCATGTT ATACTTCAAA

                3500                3520                3540
                  *
ATTATAAGTA TTATATTTAC CTTGATGATT TATTTATTAG TATATTAATT CTGATTATAA

                3560                3580                3600
                                                          *
TTATGGTGGG ATACAATCGC TTTCCACTAA ATATTTTAAC TATGATTTAT AAATTTATTT

                3620                3640                3660
CAACATCGTA TATTTACTTA TTAATACATA ATTTATCATA ATTTTATGGA AATTGAGACC

                3680                3700                3720
                                      *
```

Figure 3F

```
AAGAAACATT AAGAGAACAA ATTCTATAAC AAAGACAATT TAGAAAAAAA TGTACTTTTA

                    3740                3760                3780
GGTAATTTTA AGTACTCTTA ACCAAACACA AAAATTCAAA TCAAATGAAC TAAATAAGAT

                    3800                3820                3840
                     *
AATATAACAT ACGGAACATC TTACTTGTAA TCTTACATTC CCATAATTTT ATTATGAAAA

                    3860                3880                3900
                                                             *
ATAATCTTAT ATTACTCGAA CTAAATGTTG TCACAAATTA TTATCTAAAT AAAGAAAAAC

                    3920                3940                3960
ACTTAATTTT TATAACATTT TTTCATATAT TTGAAAGATT ATATTTTGTA TATTTACGTA

                    3980                4000                4020
                                         *
AAAATATTTG ACATAGATTG AGCACCTTCT TAACATAATC CCACCATAAG TCAAGTATGT

                    4040                4060                4080
AGATGAGAAA TTGGTACAAA CAACGTGGGG CCAAATCCCA CCAAACCATC TCTCATTCTC

                    4100                4120
                     *
TCCTATAAAA GGCTTGCTAC ACATAGACAA CAATCCACAC A CA AAT ACA CGT TCT
                                                  <Ile Cys Thr Arg

  4140                4160                4180
TTT CTT TCT ATT TGA TTA ACC ATG G CTCATAGCAT TCGTCACCCT TTCTTCCTTT
<Lys Lys Arg Asn Ser *** Gly His

      4200                4220                4240
       *
TCCAACTTTT ACTCATAAGT GTCTCACTAG TGACCGGTAG CCACACTGTT TCGGCAGCGG

      4260                4280                4300
```

Figure 3G

```
                                                                  *
CTCGACGTTT ATTCGAGACA CAAGCAACCT CATCAGAGCT CCCACAATTG GCTTCAAAAT

      4320                4340                4360
ACGAAAAGCA CGAAGAGTCT GAATACGAAA AGCCAGAATA CAAACAGCCA AAGTATCACG

      4380                4400                4420
                                *
AAGAGTACTC AAAACTTGAG AAGCCTGAAA TGCAAAAGGA GGAAAAACAA AAACCCTGCA

      4440                4460                4480
AACAGCATGA AGAGTACCAC GAGTCACACG AATCAAAGGA GCAAAAAGAG TACGAGAAAG

      4500                4520                4540
       *
AAAATCTCGA CGGGCCCGAA GATCTTCGCT AGCCGTCGAC GCCCGGGGGA ATTCGTCGAG

      4560                4580                4600
                                                 *
CCTTGAATCA TATGACGCTG GTGCATGTGC CATCATCATG CAGTAATTTC ATGGTATATC

      4620                4640                4660
GTAATATATA GTTAATAAAA AAGATGGTGA TTGGGAAATG TGTGTGTGCA TTCCTCCATG

      4680                4700                4720
                                *
CACTAATGGT GAATCTCTTT GCATACATAG AAATTCTAAA TGGTTATAGT TTATGTTATA

      4740                4760                4780
GTGTATGTTG TAGTGAAAKT AATTTTAAAT GTTGTATCTA ATGTTAACAT CACTTGGCTT

      4800                4820                4840
       *
GATTTATGTT ATGTTATGTA TTTTACTTTA ATGATATTGC ATGTATTGTT AATTTAACAT

      4860                4880                4900
                                                 *
```

Figure 3H

26027 6604680

```
TGCTTGATCA TTATACTCTT CTACTATTAA TTATAAATGG CACTGTTTTG TTTAAACTTT

      4920                4940                4960
TTACAAGTTA AGACATGTAT AAATATATGA CAATATAATT ACAAGTTTTA GTTCAATGTT

      4980                5000                5020
                           *
AGCTATCTTA GTATGTTATT GATGATCTTA ATTACATTTA AACAAATTCC ACTTAAAATT

      5040                5060                5080
TTAATAAATA ATAACAAATA ATTATTGTAA TATAATACAT TAAATGCAAC AAAAAATGAA

      5100                5120                5140
       *
ATAAATAAAA TAAAATAGCA AATAATTGTT ATAATATTGT AATATAATAT GTACCATATT

      5160                5180                5200
                                               *
CTTAACTGAA ATAGGGTCTA ACCTATAATC CCTAAAATTT CAGTTTAAAT ATTTTTATAC

      5220                5240                5260
CTGCCATATT ATTAGAACTC TTTTTAAATA TATTAAAATT TTAATTATAC CAATTTAATT

      5280                5300                5320
                           *
TAAACTATTA ATTATCTTAA CTAAAATCTA AAATTTTATT TAACCTATTA ATTAAATTCC

      5340                5360                5380
TAATTATCTT ATCTAATTTA AAACTCTAAT TATCCTAATT TGATTTAAAT TCTTGATTAT

      5400                5420                5440
       *
CTTAATTTGT AACCTCCTCC ACCCAGCTAG ATGCTGGACC CGAATCCGGG AGATTACATC

      5460                5480                5500
                                               *
GGCATTGAGA TGGCCTAGTA GTGATCAGGG TTTTCTAGAG GTACCCAATT CGCCCTATAG
```

Figure 3I

TGAGTCGT

Figure 3J

```
AAAAAACA ATG AGC ACT GCA AGA TTT ATC AAG TGT GTC ACG GTC GGT GAT     50
         Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
           1               5                  10

GGA GCT GTG GGG AAA ACT TGT ATG CTC ATT TCA TAT ACC AGC AAT ACT     98
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
 15                  20                  25                  30

TTC CCA ACG GAT TAT GTT CCA ACA GTA TTT GAT AAC TTT AGT GCC AAT    146
Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
                35                  40                  45

GTG GTG GTG GAT GGC AGC ACA GTG AAC CTT GGC CTA TGG GAC ACT GCC    194
Val Val Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
            50                  55                  60

GGG CAA GAA GAT TAT AAT AGG CTA AGG CCA CTG AGT TAT AGA GGA GCT    242
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
        65                  70                  75

GAT GTG TTT TTG TTG GCC TTT TCT CTT ATA AGC AAG GCC AGT TAT GAA    290
Asp Val Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
    80                  85                  90

AAC ATC TAC AAA AAG TGG ATC CCA GAG CTA AGA CAT TAT GCT CAT AAT    338
Asn Ile Tyr Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala His Asn
 95                  100                 105                 110

GTA CCA GTT GTG CTT GTT GGA ACC AAA CTA GAT TTG CGA GAT GAC AAG    386
Val Pro Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp Lys
                115                 120                 125

CAG TTC CTC ATT GAT CAC CCT GGA GCA ACA CCA ATA TCA ACA TCT CAG    434
Gln Phe Leu Ile Asp His Pro Gly Ala Thr Pro Ile Ser Thr Ser Gln
            130                 135                 140

GGA GAA GAA CTA AAG AAG ATG ATA GGA GCA GTT ACT TAT ATA GAA TGC    482
```

FIGURE 4A

```
Gly Glu Glu Leu Lys Lys Met Ile Gly Ala Val Thr Tyr Ile Glu Cys
       145                 150                 155

AGC TCC AAA ACC CAA CAG AAT GTG AAG GCT GTT TTC GAT GCT GCA ATA     530
Ser Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile
    160                 165                 170

AAA GTA GCT TTG AGG CCA CCA AAA CCA AAG AGA AAG CCT TGC AAA AGG     578
Lys Val Ala Leu Arg Pro Pro Lys Pro Lys Arg Lys Pro Cys Lys Arg
175                 180                 185                 190

AGA ACA TGT GCT TTC CTT TGAATATTGG ATCATTATTA CAGTCAAAAA            626
Arg Thr Cys Ala Phe Leu
                195

CAGTTAACAA AAGCTGTTGC AGATAAACAC TGAATCTGCT ATAGTTTGTT TTTGGTTTAC  686

ATATGTTCCA CGTGAAACTA TGAAGCATCT CTAAGAAAAC CCAAACTATC ATATCAACCC  746

ATCGATCAAT GAATCGATTT CAATTTTCGC AGTATAAGTT CCTTTTAATC CTTTCTTTTT  806

ACTTCATTTT ATAACGAATT CTATGGATAA TGTTCCCTAC AAACATGTCA TTACAATGTT  866

TAATTATAAA TTCCATTCTT CTATTTTACT AAAAAAAAAA AAAA                    910
```

FIGURE 4B

```
                    20                  40                  60
TTGGATGAGA ACCAATTTTT AATAGTAAAN CCTAACCAAT TTTTAATAAT AAAGCTGACT

                    80                 100                 120
                                        *
CCTAGTACAA GAGCTTTTAT TCATTCTTCT ATTTTGCTTT CCTCTAGGCT TGGCAATCGA

                   140                 160                 180
GAATTTTCTT GTGTTACAAT ATAATAAATA CATCGTAGAA ATAAATTTTA TTCAAATTGA

                   200                 220                 240
                    *
AGTCTTAACC ATCTTTAATA TTTGTAGATG TAATTTAAAT GAAAGATAAA TACATATTCT

                   260                 280                 300
                                                            *
TGGACATGTA TTTTCATCTT AATGTTTGTG GCTTTGGTGA TAGGTGTATT GATGTACGAT

                   320                 340                 360
GTCTTTTAAA TCACATATCA CATTTTGAGT TTGTATGATG ATAAGTCGAC ATAANCGAAA

                   380                 400                 420
                                        *
TATGGTGTGA TCTTCACTTT TGAACTTTGA TAAGTCACCA AACTTTAACA AAGTTTGATT

                   440                 460                 480
GTGTACATAT ATATATATAT CTTCAAATTT TATAATAAAA ATTGTGTTTA AATAATTTAC

                   500                 520                 540
                    *
AGTTATATTA TTTTTTTATC TCTAATTTTA TTTGTCGCCA AATTTTTAGT TGATATTTTA

                   560                 580                 600
                                                            *
ACATAAAAAA AATTGTACAC ATTTACAAGC CCATATACAA ATAATTATAT AAATATTCAT
```

FIGURE 5/A

```
                    620                 640                 660
TAAAAAATAT ATTTAAATAT AGGATATAAA TATAACTATT TTAGAATTAT TCTACTTTAA

                    680                 700                 720
                                        *
GATAACATAG GTTAAATGTA TAATTAATAA GGTTAGTTTA TTGTAAAGAT GAGTATATAT

                    740                 760                 780
GTCGTAAACA TAATCACTAA CCATTTTTAT TAACTTCTTG GTTTTGAAGT TCCAAAAAGA

                    800                 820                 840
                    *
AAATGGAAGG GAAATTTGAG AGTAAGTTCA TGTTTATATT ATACATAATG AAGTTGATGT

                    860                 880                 900
                                                            *
TTTCTTCTTT TTAATATTTT TATACAAAAT ATTTAAATAA AATAATTAAG GATTGAATGA

                    920                 940                 960
AAAATATAAT GAAAGTCGTT TTACTAATAG TCATATTGCA TTTTGTCGCA TCTACTTAAA

                    980                 1000                1020
                                        *
TAATAGATAA ATTAATTGTG GTACATTAGA TCAAAGAACA AACTAGATTT TGTCCCATTC

                    1040                1060                1080
TATTGTTAAA AGCTGGTCCG TTTACATTAA AATAAGGTAC ATGTTACATG CCACGTATAA

                    1100                1120                1140
                    *
CTATCTGGTT ATTCTATCAA TCACGGTAAT TTTTAACAGT AGAAATGAAT GTAATTTTTA

                    1160                1180                1200
                                                            *
AATAGAAAGG GTCAAATTGT TATTTGATCT AACACGTAGG GATTAATTTA CTTATTTTCC

                    1220                1240                1260
```

FIGURE 5/B

```
TAAAGAAATA AGTAAAATAT AATTTGAATC TTAATACAAA AACTTTCATG ATACTTTTAT

                  1280                1300                1320
                                      *
CATATTTTAC TTATAATTTA ATATTGTGAG AGTAACAAAR TTAAAAAACA TAGAAACACC

                  1340                1360                1380
AAAAGTTAGT TATGGTGTGA CTCATATACA CAGTTAAAAT TTGAATAAAT TTTTTTCTTC

                  1400                1420                1440
                  *
GTCATTAATT CCATCATGGG TTTTTTTTTT TCTAGTTAAG CCATAATTAT CAAAATAATC

                  1460                1480                1500
                                                          *
ATCATTAATC CTATCAATAC CCCGCCCTGC CTCCCTCCCT CAATACTTAA ACCCAACTAA

                  1520                1540                1560
CACCCAGCAC CAAACGCACT TTAATAGCCA CCTATTTCTA GCCATGTCCT TGCACTTAAA

                  1580                1600                1620
                                      *
GAAAAGTAAA GCTAACCTGC AATCATTCCA TATCGAGGCC TCAACAGATA AAGTTGGTTG

                  1640                1660                1680
ATGGGTTTGC ACCAAGTTGT TAAAACCCGG CCCTCAACTT CCCTTTTCTT TTCATCCTCC

                  1700                1720                1740
                  *
CCACTCCACA CCCTCCAATT TTCTTCATAT GGTTCTATTA TAAGTTCTTT ATAATCACAG

                  1760                1780                1800
                                                          *
AATCAAGATA AGTCCTCAGC AAACAAAAAA CCATGGCTCT CGAGCAAGAT CTGGACTAGT

                  1820                1840                1860
CAGAGCTCTG AATATTGGAT CATTATTACA GTCAAAAACA GTTAACAAAA GCTGTTGCAG
```

FIGURE 5/C

```
                1880                1900                1920
                                     *
ATAAACACTG AATCTGCTAT AGTTTGTTTT TGGTTTACAT ATGTTCCACG TGAAACTATG

                1940                1960                1980
AAGCATCTCT AAGAAAACCC AAACTATCAT ATCAACCCAT CGATCAATGA ATCGATTTCA

                2000                2020                2040
                 *
ATTTTCGCAG TATAAGTTCC TTTTAATCCT TTCTTTTTAC TTCATTTTAT AACGAATTCT

                2060                2080                2100
                                                         *
ATGGATAATG TTCCCTACAA ACATGTCATT ACAATGTTTA ATTATAAATT CCATTCTTCT

                2120                2140                2160
ATTTTACTAA GATATTAGTA ACTTCAAACT GCTGATTTTT ACTAATTTAT TATTTATAAA

                2180                2200                2220
                                     *
TTGTTAGAAT GATTATTTTT CAATAATTTA ACAACAATAT TTAATATTAT TATTATTATT

                2240                2260                2280
ATTTCTCAAT TTTTATTAAA CAAAAACATA AATTTTTGAC AAATTAAAAT AAATGAATTA

                2300                2320                2340
                 *
ATTTCTCAAT TTTTCGTGCA ACTATTACAA AAATCCTTCA TAGTCCTAAT CTTAATTTGA

                2360                2380                2400
                                                         *
TGCAGAGGTG ATAATAATCT TAATTTGATG CAGAGGTAAT AATGGGCCGG GTTTGAGCTG

                2420                2440                2460
GACTTAAGCA TGATATTGAC GTACTTTATA TTTTTCCAAA TTCAACCCAG CTCGAAATAT
```

FIGURE 5/D

```
                    2480                2500                2520
                                         *
GAGTCTAAAA TTTTGTCCAA TTTAATCCAA GCCCATTTTA AGTTCGTCCA TATTATTTTT

                    2540                2560                2580
TAATTTAAAA AATTTATATC ATTTTATTTT AATATTTAAT TATTTTATAT ATTTTTTATT

                    2600                2620                2640
                     *
TATTGAAAAT TTTTATATAG TCATCTTAAC ATTATGTTAA TGTTTATATT AGAGTAGTAT

                    2660                2680                2700
                                                             *
TATATATATT TAGTATAGGT TTATTTTGTT AATAAACTTA AAAATGGGTC TTGTGGGCTA

                    2720                2740                2760
GACTTGGACC TTAAATGCTC AAACTCAAAC TTAATTCATA TTTTAAACAG GCTTAATATT

                    2780                2800                2820
                                         *
TTTATTTACA CTGTTTCAAA TTTTTCGGGT GAAATATCTT CGAGTCTAGA TTAATAACAC

                    2840                2860                2880
CACAGGTCTA ATTTGATGCT CAATGAAAAT GAAATCATAT TGAGCTTAAT TAATATTCCA

                    2900                2920                2940
                     *
TTCTTCTTTG CTGAAAGGAC CAAGCAATTC GAGTTACATT AAGGTTAAAG AGTATGGGAT

                    2960                2980                3000
                                                             *
CCGCCAAACC TGCCCCAATG TCTCTTCAAC CATCCAAAAA CTTGAGTCAG TATCACATAC

                    3020                3040
ATGTACCGNT ATTTATTTAT TTATTGAAAT TGGCATTATT TCTTG
```

FIGURE 5/E

Sequence: 5 of 5 Software: 4.2.0.5

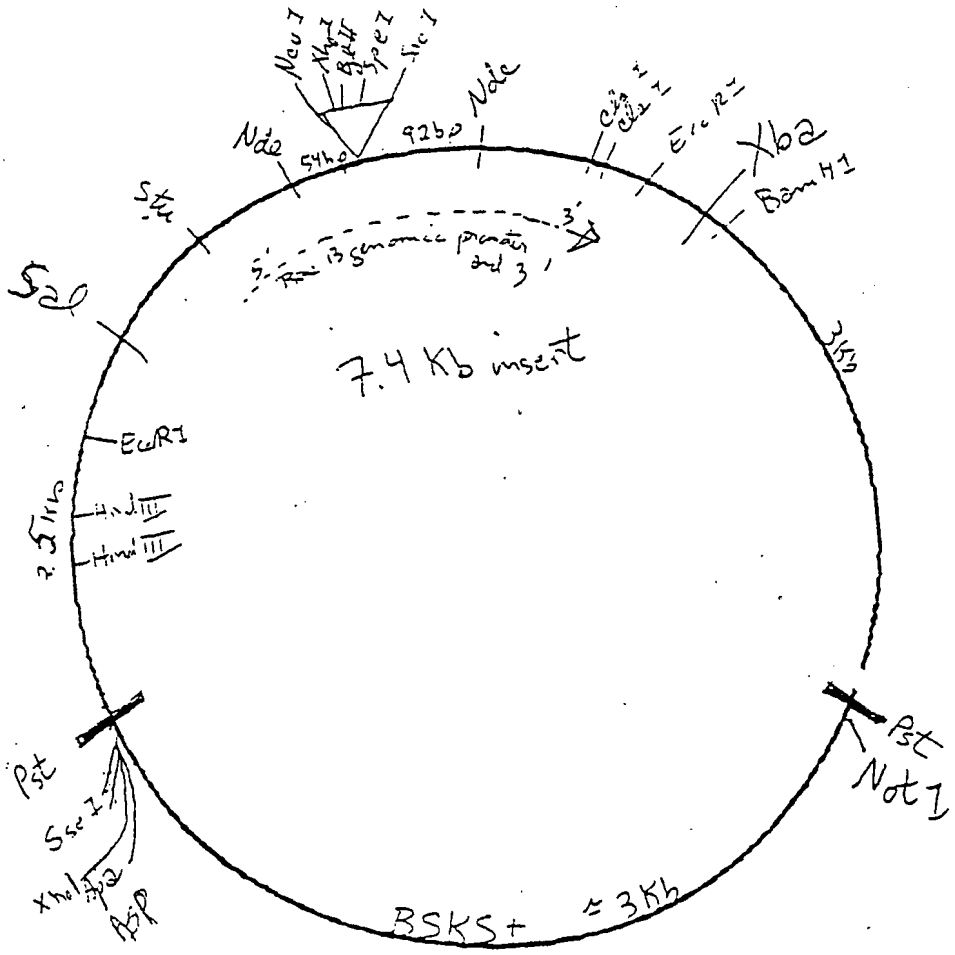


FIGURE 6

GGGCATTCCA CACGACCATG TGTCCCCTAT TTCCAGGCAT TTTGAGACTT CACCTAAACT 60

TCTAGAGTTG TTTCAAATTA GCCCCTATTT GTTCTTAAAT CATTTTAGGA TCTTGTAAAC 120

TCGTATTTAG GACTAAATGT GTAATTTATA CTTTAATTAT GATTGATTAA TTGATTGATT 180

TNGTAGTAAT GCCCGTGACC CTAATCCGTT AGCGAAGAGG GGTTAGGGGT TAGGGGTTTT 240

ATTATTATTT TTTAGATATT GTATAACTCT TGTTTTATTT TTAATTTTGT TACTATTTCA 300

AAGGCATTTG TTTGTAGTGT TATTTCGAGT AGGTTTTATG GGTGAACAAC CCTTGACCGC 360

CAAATCAATC ACAAGAGTTC AACATTTTAT TTATTTTGAA ATGTATTAAA AATCGTTAAT 420

CTATATATTC GCCCCATTAT TGGGATTAAA TATTCACAAG GGTTTAGACC GTCATGAGAC 480

AGATTAGTTT TATCTTACTG ATGGTCACAT CACAATAGTA ATTCAACTTA ATACGAGAGG 540

AACCATTGAT TCACGCAATT GGTCATCGCA CTTAGTTGAA AAGCTAGGGG TGCGAAGCTA 600

CCGTACGCTG GATTATGATT GAACACCTCT AAGTCAGAAT CCGAATTAGA AACAATGCAC 660

GTGTCCGTTG CCTGATTGCC AACCCCAATA ACACGTGTTG TAGGTTTAAC CATGTTTATG 720

AAAGATAAGG TTTTTTTTTT TATAAGCAAG CAACTATAGG GGTTTACTTC CGTGCGCAAA 780

TTTTTAGGTT ACCTATTTTG GGAGGGGGGA TTATGATTCA AGTGAAAGAA AGTTGGCACA 840

CACACAATCA GTACATCTGT TTTGACAGAG ACACAGCCTA AAAACAGCAG CAAACAAGCC 900

TAAAGGAATC ACCCAAAAAC AACAACCAAA AGTACAGAGG AAAACAAAAG AATCCCTGTT 960

ACCACCAAGC TGAAAAAAAG AAAATAAAAC TCAACTTTTG GCAATAAAAA CCCTCCTACC 1020

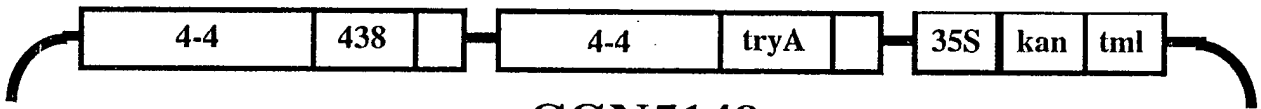
CTCAACCCCT AACCACGCAA CAATCAGCAA TACTCCAAGC AACCATTTTC CTTACAAGTT 1080

FIGURE 7A

```
TGTTTTTCTT GTGATTAATC CAT ATG GCT AGC TCC ATG TCC CTT AAG CTT GCA 1133
                          Met Ala Ser Ser Met Ser Leu Lys Leu Ala>

TGT CTG CTA GTG TTG TGC ATG GTG GTG GGT GCA CCC CTG GCT CAA GGG   1181
Cys Leu Leu Val Leu Cys Met Val Val Gly Ala Pro Leu Ala Gln Gly>

GAC GTA ACC CGT GCT GAT GGC GTA GTC ACC CTT CCA CGC TGC CTT CCT   1229
Asp Val Thr Arg Ala Asp Gly Val Val Thr Leu Pro Arg Cys Leu Pro>

TTA TTG ATA GGG AAT GGT AAT GGT GCT GAT GCT GAT GTT GAT GCC CCA   1277
Leu Leu Ile Gly Asn Gly Asn Gly Ala Asp Ala Asp Val Asp Ala Pro>

GCT TGC TGC GAC ATC GTC AGG GGT CTC TTG AGC TCG CTG CTC TGT GGT   1325
Ala Cys Cys Asp Ile Val Arg Gly Leu Leu Ser Ser Leu Leu Cys Gly>

GGT GTT TAGGAACCG ATCTAGCTTG AAATCGGGTT CGGATACGGG TGGAGTTTCA     1380
Gly Val>

AATTGGTGTG TTATGGAATC CCAACTTAAT CGTGTTTAGG GGTGGGATCC AATTGTGTGA 1440

TACATTACAG AGCATGGTTG TGGATTGTTT TCTCATATGT TTTGATTGAC TTGCTTGATA 1500

CATTGGATGA TTCGATAAGG TGACCGGTTT ACCTGGGTAT CCAACCATCA TCCGATTACT 1560

TTTTAATAAT TATTTGTTTC TTCTTTATGT TGTCTGTCTT TTTGTTTCTT GATCTATAAC 1620

ATTATATTTG CCCAAATTTT CGCATTTTCC ATATGTAGCT TATATATGTA TATATATATT 1680

CAATAAAGTA TATTGATTTA GCAGATGATT TGTGTATATA TTTAAATCAA ATCAAACATT 1740

AATGATCATT CACTAGCGTC TTAATCTTGA AAAATTCATC AACGGTTATC CTTTGCAGCA 1800

TATATAAAAA AAATTGCCAA CCCTATGCTT TTACACCTAA TTCAAGGGAT AACATAAGTC 1860

GATTAAAACG A                                                     1871
```

FIGURE 7B

26027 6604868



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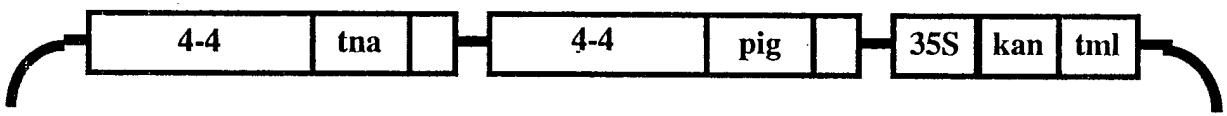

pCGN5616

FIGURE 8

26027 6607680

Coker 130	Yxy, Y	Yxy, x	Yxy, y	Lab, L	Lab,a	Lab,b	LCh, L	LCh,C	LCh, h
1	80.35	.3206	0.3266	91.84	0.16	5.51	91.84	5.51	88.4
2	77.62	.3232	0.3282	90.6	0.66	6.45	90.6	6.48	84.2
3	80.98	.3197	0.3257	92.12	0.13	5.04	92.12	5.04	88.6
4	80.16	.3200	0.3255	91.75	0.35	5.00	91.75	5.01	86.1
5	77.03	.3220	0.3271	90.33	0.61	5.84	90.33	5.87	84.1
6	73.67	.3258	0.3293	88.76	1.35	7.14	88.76	7.26	79.4
7	82.43	.3178	0.3237	92.76	0.15	4.05	92.76	4.05	87.9
8	82.21	.3196	0.3255	92.66	0.19	4.99	92.66	4.99	87.9
9	81.19	.3194	0.3241	92.21	0.77	4.42	92.21	4.48	80.2
10	76.11	.3243	0.329	89.9	0.74	6.89	89.9	6.92	84
11	82.28	.3178	0.3236	92.69	0.19	4.00	92.69	4.00	87.3
TOTAL	874.03	3.5302	3.5883	1005.62	5.30	59.33	1005.62	59.61	938.10
MEAN	79.46	.3209	.3262	91.42	0.48	5.39	91.42	5.42	85.28
S.D.	2.91	.0026	.0020	1.33	0.38	1.08	1.33	1.11	3.22
RANGE	82.43-73.67	.3858-.3178	0.3293-.3236	92.76-88.76	1.35-.13	7.14-4.00	92.76-88.76	7.26-4.00	88.6-79.4
AVER DEV.	2.44	.0021	.0017	1.11	0.31	0.88	1.11	0.90	2.64

Coker 130	Hunter L	Hunter a	Hunter B
1	89.63	0.15	5.42
2	88.10	0.66	6.27
3	89.98	0.13	4.98
4	89.53	0.36	4.94
5	87.76	0.61	5.69
6	85.83	1.35	6.85
7	90.79	0.15	4.03
8	90.67	0.19	4.95
9	90.10	0.78	4.38
10	87.23	0.75	6.65
11	90.70	0.19	3.98
TOTAL	980.32	5.32	58.14
MEAN	89.12	0.48	5.29
S.D.	1.65	0.39	0.99
RANGE	90.79-85.83	1.35-.13	6.85-3.98
AVER DEV.	1.37	0.31	0.81

FIGURE 9

2602F 660h8680

5148	Yxy, Y	Yxy, x	Yxy, y	Lab, L	Lab,a	Lab,b	LCh, L	LCh,C	LCh, h
68-1	60.76	0.34	0.35	82.24	2.32	15.11	82.24	15.28	81.3
68-1	61.89	0.34	0.34	82.82	1.97	14.31	82.85	14.44	82.2
50-2-1	78.39	0.3324	0.3375	90.95	0.68	11.29	90.95	11.31	86.6
50-2-1									
(lint fiber)	21.49	.3155	0.3489	53.48	-8.01	7.97	53.48	11.29	135.2
5148	Hunter L	Hunter a	Hunter B						
68-1	77.94	2.25	13.35						
68-1	78.67	1.92	12.75						
50-2-1	88.53	0.69	10.71						
50-2-1									
(lint fiber)	46.35	-6.35	6.06						
				FIGURE 10					

26E02T* 660h8680

5149	Yxy, Y	Yxy, x	Yxy, y	Lab, L	Lab,a	Lab,b	LCh, L	LCh,C	LCh, h
68-1	65.75	0.3351	0.34	84.86	0.72	11.9	84.86	11.92	86.6
68-1	62.54	.3458	0.3474	83.19	2.14	15.84	83.19	15.98	82.4
68-1	62.56	0.3458	0.3474	83.2	2.14	15.85	83.2	15.99	82.4
8-1	84.72	.3196	0.3278	93.76	0.89	5.87	93.76	5.93	98.6
68-1	64.97	.3316	0.3354	84.46	1.17	9.81	84.46	9.87	83.3
17-2	64.42	.3423	0.3436	84.18	2.26	14.19	84.18	14.36	81
17-3	60.97	.3475	0.3475	82.36	2.74	16.03	82.36	16.26	80.4
17-15-1	64.02	.3433	0.3444	83.97	2.34	14.57	83.97	14.75	80.9
21-1	59.32	0.3443	0.3445	81.46	2.64	14.41	81.46	14.64	79.7
21-3	63.64	0.34	0.3409	83.77	2.4	12.89	83.77	13.11	79.5
21-6	67.12	0.3372	0.3394	85.56	1.88	12.15	85.56	12.29	81.3
50-3-1	61.26	0.3502	0.3511	82.51	2.4	17.63	82.51	17.79	82.3
67-1	64.34	0.3434	0.3442	84.13	2.48	14.58	84.13	14.78	80.4
68-1	64.12	0.3442	0.3447	84.02	2.58	14.85	84.02	15.07	80.2
68-2	70.21	0.3428	0.3447	87.09	2.05	15.04	87.09	15.17	82.3
68-3	63.81	0.3457	0.3468	83.86	2.35	15.76	83.86	15.93	81.6

5149	Hunter L	Hunter a	Hunter B
68-1	81.08	0.71	10.89
68-1	79.08	2.08	14
68-1	79.09	2.09	14.02
8-1	92.04	0.91	5.81
68-1	80.6	1.15	9.06
17-2	80.25	2.21	12.75
17-3	78.08	2.68	14.09
17-15-1	80.01	2.29	13.05
21-1	77.01	2.56	12.73
21-3	79.77	2.35	11.65
21-6	81.92	1.86	11.14
50-3-1	78.26	2.33	15.36
67-1	80.2	2.43	13.07
68-1	80.07	2.53	13.28
68-2	83.79	2.04	13.68
68-3	79.87	2.3	14

FIGURE 11

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5616	Yxy, Y	Yxy, x	Yxy, y	Lab, L	Lab,a	Lab,b	LCh, L	LCh,C	LCh, h
11-1	72.26	0.3215	0.3254	88.09	1.1	5.06	88.09	5.17	77.8
11-2	58.69	0.3284	0.3335	81.12	0.6	8.36	81.12	8.38	85.9
11-2	52.78	0.3358	0.3335	77.74	3.55	9.22	77.74	9.87	69
11-1	72.03	0.3312	0.3338	87.98	1.72	9.52	87.98	9.67	79.8
11-1	72.34	0.3295	0.332	88.13	1.79	8.64	88.13	8.82	78.4
11-1	71.98	0.3295	0.3313	87.95	2.09	8.39	87.95	8.64	76.1
11-1	73.01	0.3256	0.3305	88.45	0.68	7.51	88.45	7.54	84.9
17-1-2	75.85	0.3274	0.3306	89.78	1.52	7.94	89.78	8.08	79.3
17-3-1	72.6	0.3271	0.3303	88.25	1.48	7.66	88.25	7.8	79.1
17-4-1	69.02	0.3352	0.3377	86.51	1.78	11.37	86.51	11.5	81.2
25-11-1	69.5	0.3364	0.3401	86.75	1.26	12.41	86.75	12.47	84.2
25-28-1	72.21	0.3324	0.3343	88.06	2.09	9.9	88.06	10.11	78.2
25-36-2	70.46	0.3327	0.3353	87.22	1.73	10.22	87.22	10.36	80.5
35-35-1	75.59	0.3268	0.3299	89.66	1.56	7.58	89.66	7.73	78.4
50-12-1	73.13	0.3284	0.3316	88.5	1.46	8.36	88.5	8.48	80.1
KS-11-2	65.33	0.3371	0.3388	84.65	2.07	11.83	84.65	12	80.1

5616	Hunter L	Hunter a	Hunter B
11-1	85	1.09	4.89
11-2	76.61	0.58	7.64
11-2	72.64	3.38	8.22
11-1	84.87	1.72	8.97
11-1	85.05	1.79	8.2
11-1	84.84	2.08	7.96
11-1	85.44	0.67	7.18
17-1-2	87.08	1.52	7.62
17-3-1	85.2	1.48	7.31
17-4-1	83.07	1.76	10.52
25-11-1	83.36	1.25	11.43
25-28-1	84.97	2.08	9.32
25-36-2	83.94	1.72	9.56
35-35-1	86.94	1.57	7.29
50-12-1	85.51	1.46	7.96
KS-11-2	80.82	2.04	10.81

FIGURE 12

26E02T* 660h868

BC	Yxy, Y	Yxy, x	Yxy, y	Lab, L	Lab,a	Lab,b	LCh, L	LCh,C	LCh, h
12 Green	33.34	0.3779	0.3717	66.01	4.24	24.18	66.01	24.54	80.1
22 Brown	38.18	0.3778	0.3662	68.15	6.18	23.31	68.15	24.11	75.2
3 Red	24.23	0.4055	0.3728	56.31	10.96	25.52	56.31	27.77	66.9
4 Ivory	46.84	0.3657	0.3599	74.08	4.6	21.13	74.08	21.62	77.8

BC	Hunter L	Hunter a	Hunter B
12 Green	59.44	3.79	17.92
22 Brown	61.78	5.62	17.69
3 Red	49.22	9.42	17.14
4 Ivory	68.43	4.31	17.02

FIGURE 13